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RAW SEQUENCE LISTING   DATE: 01/15/2002
PATENT APPLICATION: US/09/892,227   TIME: 15:12:46

Input Set : N:\Crf3\RULE60\09892227.txt
Output Set: N:\CRF3\01152002\I892227.raw

SEQUENCE LISTING

ENTERED

```
 3 (1) GENERAL INFORMATION:
 4      (i) APPLICANT: Gossen, Manfred
 5                     Bujard, Hermann
 6                     Salfeld, Jochen
 7                     Voss, Jeffrey
 9     (ii) TITLE OF INVENTION: Animal Transgenic for a Tetracycline-Controlled
10                              Transcriptiona
11    (iii) NUMBER OF SEQUENCES: 10
12     (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: Lahive & Cockfield
15          (B) STREET: 60 State Street, Suite 510
16          (C) CITY: Boston
17          (D) STATE: Massachusetts
18          (E) COUNTRY: USA
19          (F) ZIP: 02109-1875
20      (v) COMPUTER READABLE FORM:
21          (A) MEDIUM TYPE: Floppy disk
22          (B) COMPUTER: IBM PC compatible
23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24          (D) SOFTWARE: ASCII text
26     (vi) CURRENT APPLICATION DATA:
27          (A) APPLICATION NUMBER: US/09/892,227      C-->
28          (B) FILING DATE: 25-Jun-2001              C-->
29          (C) CLASSIFICATION:
30    (vii) PRIOR APPLICATION DATA:
32          (A) APPLICATION NUMBER: 09/163,269
33          (B) FILING DATE:
35          (A) APPLICATION NUMBER: 08/076,327
37          (B) FILING DATE: 14-JUN-1993
38   (viii) ATTORNEY/AGENT INFORMATION:
39          (A) NAME: Giulio A. DeConti, Jr.
40          (B) REGISTRATION NUMBER: 31,503
41          (C) REFERENCE/DOCKET NUMBER: BBI-013CP2
42     (ix) TELECOMMUNICATION INFORMATION:
43          (A) TELEPHONE: (617) 227-7400
44          (B) TELEFAX: (617) 227-5941
46 (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1008 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: double
52          (D) TOPOLOGY: linear
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```
54      (ii) MOLECULE TYPE: DNA (genomic)
56      (vi) ORIGINAL SOURCE:
57            (A) ORGANISM: Herpes Simplex Virus
58            (B) STRAIN: K12, KOS
60     (vii) IMMEDIATE SOURCE:
61            (B) CLONE: tTA transactivator
63      (ix) FEATURE:
64            (A) NAME/KEY: exon
65            (B) LOCATION: 1..1008
67      (ix) FEATURE:
68            (A) NAME/KEY: mRNA
69            (B) LOCATION: 1..1008
71      (ix) FEATURE:
72            (A) NAME/KEY: misc. binding
73            (B) LOCATION: 1..207
75      (ix) FEATURE:
76            (A) NAME/KEY: misc. binding
77            (B) LOCATION: 208..335
79      (ix) FEATURE:
80            (A) NAME/KEY: CDS
81            (B) LOCATION: 1..1005
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
84  ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG    48
85  Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
86   1               5                  10                  15
88  CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG    96
89  Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
90                  20                  25                  30
92  AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG    144
93  Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
94          35                  40                  45
96  CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT    192
97  Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
98      50                  55                  60
100 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT    240
101 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
102 65                  70                  75                  80
104 AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA    288
105 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
106                 85                  90                  95
108 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT    336
109 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
110                 100                 105                 110
112 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG    384
113 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
114                 115                 120                 125
116 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC    432
117 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
118         130                 135                 140
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120 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA   480
121 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
122 145             150             155             160
124 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA   528
125 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
126             165             170             175
128 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG   576
129 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
130             180             185             190
132 ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG   624
133 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
134             195             200             205
136 TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC   672
137 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
138             210             215             220
140 CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG   720
141 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
142 225             230             235             240
144 GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG   768
145 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
146             245             250             255
148 ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC   816
149 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
150             260             265             270
152 GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT   864
153 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
154             275             280             285
156 CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC   912
157 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
158 290             295             300
160 CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT   960
161 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
162 305             310             315             320
164 GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG  1008
165 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
166             325             330             335
168 (2) INFORMATION FOR SEQ ID NO: 2:
169      (i) SEQUENCE CHARACTERISTICS:
170          (A) LENGTH: 335 amino acids
171          (B) TYPE: amino acid
172          (D) TOPOLOGY: linear
173      (ii) MOLECULE TYPE: protein
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
175 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
176   1             5             10             15
178 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
179             20             25             30
181 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
182             35             40             45
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```
184 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
185      50                  55                  60
187 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
188  65                  70                  75                  80
190 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
191                  85                  90                  95
193 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
194                 100                 105                 110
196 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
197             115                 120                 125
199 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
200         130                 135                 140
202 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
203 145                 150                 155                 160
205 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
206                 165                 170                 175
208 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
209                 180                 185                 190
211 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
212             195                 200                 205
214 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
215         210                 215                 220
217 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
218 225                 230                 235                 240
220 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
221                 245                 250                 255
223 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
224             260                 265                 270
226 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
227         275                 280                 285
229 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
230     290                 295                 300
232 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
233 305                 310                 315                 320
235 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
236             325                 330                 335
239 (2) INFORMATION FOR SEQ ID NO: 3:
240      (i) SEQUENCE CHARACTERISTICS:
241          (A) LENGTH: 894 base pairs
242          (B) TYPE: nucleic acid
243          (C) STRANDEDNESS: double
244          (D) TOPOLOGY: linear
246     (ii) MOLECULE TYPE: DNA (genomic)
248     (vi) ORIGINAL SOURCE:
249          (A) ORGANISM: Herpes Simplex Virus
250          (B) STRAIN: K12, KOS
251          (C) INDIVIDUAL ISOLATE: tTAS transactivator
253     (ix) FEATURE:
254          (A) NAME/KEY: exon
```

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Output Set: N:\CRF3\01152002\I892227.raw

```
255            (B) LOCATION: 1..894
257     (ix) FEATURE:
258            (A) NAME/KEY: mRNA
259            (B) LOCATION: 1..894
261     (ix) FEATURE:
262            (A) NAME/KEY: misc. binding
263            (B) LOCATION: 1..207
265     (ix) FEATURE:
266            (A) NAME/KEY: misc. binding
267            (B) LOCATION: 208..297
269     (ix) FEATURE:
270            (A) NAME/KEY: CDS
271            (B) LOCATION: 1..891
273     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
274 ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG    48
275 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
276   1               5                  10                  15
277 CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG    96
278 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
279              20                  25                  30
280 AAG CTA GGT GTA GAG CAG CCT ACA TTG TAT TGG CAT GTA AAA AAT AAG   144
281 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
282              35                  40                  45
283 CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT   192
284 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
285     50                  55                  60
286 ACT CAC TTT TGC CCT TTA GAA GGG GAA AGC TGG CAA GAT TTT TTA CGT   240
287 Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
288  65                  70                  75                  80
289 AAT AAC GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC GAT GGA   288
290 Asn Asn Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
291              85                  90                  95
292 GCA AAA GTA CAT TTA GGT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT   336
293 Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
294             100                 105                 110
295 CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG   384
296 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
297             115                 120                 125
298 AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC   432
299 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
300             130                 135                 140
301 GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA   480
302 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
303 145                 150                 155                 160
304 CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA   528
305 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
306             165                 170                 175
307 TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG   576
308 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/892,227

DATE: 01/15/2002
TIME: 15:12:47

Input Set : N:\Crf3\RULE60\09892227.txt
Output Set: N:\CRF3\01152002\I892227.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]